



00001700 J070202

#6

## SEQUENCE LISTING

<110> Dunn-Coleman, Nigel  
Langdon, Timothy  
Morse, Phillip

<120> Manipulation of the Phenolic Acid  
Content and Digestibility of Plant Cell Walls by Targeted  
Expression of Genes Encoding Cell Wall Degrading Enzymes

<130> GC648-2

<140> US 09/991,209

<141> 2001-11-16

<150> US 60/249,608

<151> 2000-11-17

<160> 97

<170> FastSEQ for Windows Version 4.0

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<211> 2436

<212> DNA

<213> Aspergillus niger

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 Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu  
 65 70 75 80  
 Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp  
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 Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp  
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 Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly  
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<220>  
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[illegible]



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<210> 42  
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<220>  
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 35          40          45
Glu Asp Leu Tyr Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala
 50          55          60
Ala Tyr Ala Asp Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu
 65          70          75          80
Lys Ile Tyr Asn Ser Gln Thr Asp Ile Asn Gly Trp Ile Leu Arg Asp
 85          90          95
Asp Ser Ser Lys Glu Ile Ile Thr Val Phe Arg Gly Thr Gly Ser Asp
100          105          110
Thr Asn Leu Gln Leu Asp Thr Asn Tyr Thr Leu Thr Pro Phe Asp Thr
115          120          125
Leu Pro Gln Cys Asn Gly Cys Glu Val His Gly Gly Tyr Tyr Ile Gly
130          135          140
Trp Val Ser Val Gln Asp Gln Val Glu Ser Leu Val Lys Gln Gln Val
145          150          155          160
Ser Gln Tyr Pro Asp Tyr Ala Leu Thr Val Thr Gly His Xaa Leu Gly
165          170          175
Ala Ser Leu Ala Ala Leu Thr Ala Ala Gln Leu Ser Ala Thr Tyr Asp
180          185          190
Asn Ile Arg Leu Tyr Thr Phe Gly Glu Pro Arg Ser Gly Asn Gln Ala
195          200          205
Phe Ala Ser Tyr Met Asn Asp Ala Phe Gln Ala Ser Ser Pro Asp Thr
210          215          220
Thr Gln Tyr Phe Arg Val Thr His Ala Asn Asp Gly Ile Pro Asn Leu
225          230          235          240
Pro Pro Val Glu Gln Gly Tyr Ala His Gly Gly Val Glu Tyr Trp Ser
245          250          255
Val Asp Pro Tyr Ser Ala Gln Asn Thr Phe Val Cys Thr Gly Asp Glu
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<210> 43  
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<220>  
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<210> 44  
 <211> 27  
 <212> PRT  
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<220>  
 <223> aleurain-NPIR delete structure

<400> 44  
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 Ala Ala Val Ala Val Ala Ser Ser Arg Ala Ala  
 20 25

<210> 45  
 <211> 93  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> aleurain-NPIR delete structure encoding sequence

<400> 45  
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 gccgtcgccg tcgcctcttc ccgcgcggcc gcc 93



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<211> 40

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> primer

<400> 49

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<210> 50

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<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> primer

<400> 50

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35

<210> 51

<211> 44

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> primer

<400> 51

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44

<210> 52

<211> 50

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$ 

<223> primer

<400> 52

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<211> 325  
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 gttatttatg agatggggtt ttatgattag agtcccgcga ttatacattt aatacgcgat 240  
 agaaaacaaa atatagcgcg caaactagga taaattatcg cgcgcggtgt catctatggt 300  
 actagatcga taagcttcta gatct 325

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 <211> 72  
 <212> DNA  
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<220>  
 <223> primer

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<220>  
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<400> 55  
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<210> 56  
 <211> 40  
 <212> DNA  
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<220>  
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<400> 56  
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 <211> 33  
 <212> DNA  
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<220>  
 <223> primer

<400> 57  
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<220>  
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<400> 65  
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<400> 66  
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<220>  
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<400> 67  
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<210> 68  
 <211> 54  
 <212> DNA  
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<220>  
 <223> primer

<400> 68



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<210> 70  
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<220>  
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<400> 70  
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<210> 71  
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<220>  
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<210> 77  
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<210> 78  
 <211> 37  
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<220>  
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<400> 78  
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<210> 79  
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<400> 79  
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<400> 84

gtaggtag 8

<210> 85

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Lys Pro Leu Lys Asp Glu Leu  
1 5

<210> 86

<211> 7

<212> PRT

<213> Artificial Sequence

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<223> designated KDEL fusion peptide

<400> 86

Glu Pro Leu Lys Asp Glu Leu  
1 5

<210> 87

<211> 5

<212> PRT

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<223> frameshifted terminal peptide

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Glu Thr Thr Glu Gly  
1 5

<210> 88

<211> 27

<212> PRT

<213> Aspergillus niger

<400> 88

Met Lys Gln Phe Ser Ala Lys His Val Leu Ala Val Val Val Thr Ala  
1 5 10 15  
Gly His Ala Leu Ala Ala Ser Thr Gln Gly Ile  
20 25

<210> 89

<211> 9

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<213> Aspergillus niger

<400> 89

Met Ala Ala Ala Ser Thr Gln Gly Ile  
1 5

<210> 90

<211> 7

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<213> Artificial Sequence

<220>

<223> ER retention vector

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Lys Pro Leu Lys Asp Glu Leu  
1 5

<210> 91  
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<212> PRT  
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<220>  
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<400> 91  
Pro Val Ala Ala Ala  
1 5

<210> 92  
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<212> DNA  
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<220>  
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<400> 92  
tatccatggc ggccgcgcgg tcggtgacgg gccggccccg gttggagtcg gcgaa 55

<210> 93  
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<212> PRT  
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<220>  
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<400> 93  
Cys Thr Trp Pro Val Ala Ala Ala  
1 5

<210> 94  
<211> 72  
<212> PRT  
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<220>  
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<400> 94  
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1 5 10 15  
Gly His Ala Leu Ala Ala Ser Thr Gln Gly Ile Ser Glu Asp Leu Tyr  
20 25 30  
Ser Arg Leu Val Glu Met Ala Thr Ile Ser Gln Ala Ala Tyr Ala Asp  
35 40 45  
Leu Cys Asn Ile Pro Ser Thr Ile Ile Lys Gly Glu Lys Ile Tyr Asn  
50 55 60  
Ser Gln Thr Asp Ile Asn Gly Trp  
65 70

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<400> 95
Tyr Ala Leu Thr Val Thr Gly His Ser Leu Gly Ala Ser Leu Ala Ala
 1             5             10            15
Leu
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<210> 96
<211> 17
<212> PRT
<213> Artificial Sequence
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<400> 96
Tyr Ala Leu Thr Val Thr Gly His Ala Leu Gly Ala Ser Leu Ala Ala
 1             5             10            15
Leu
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<210> 97
<211> 4
<212> PRT
<213> Artificial Sequence
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<400> 97  
Lys Asp Glu Leu  
1